

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/089,211B

Source: 1FW16

Date Processed by STIC: 11/9/04

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 11/09/2004

PATENT APPLICATION: US/10/089,211B

TIME: 12:46:43

Input Set : A:\62447-01.ST25.txt

Output Set: N:\CRF4\11092004\J089211B.raw

3 <110> APPLICANT: University of Victoria Innovation and Developement  
 4 Corporation  
 5 Hintz, William E.  
 6 Eades, Caleb Joshua  
 8 <120> TITLE OF INVENTION: Mannosidases and Methods for using the Same  
 10 <130> FILE REFERENCE: 2847-62447-01  
 12 <140> CURRENT APPLICATION NUMBER: 10/089,211B  
 13 <141> CURRENT FILING DATE: 2002-03-25  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US00/27210  
 16 <151> PRIOR FILING DATE: 2000-10-02  
 18 <150> PRIOR APPLICATION NUMBER: 60/157,341  
 19 <151> PRIOR FILING DATE: 1999-10-01  
 21 <160> NUMBER OF SEQ ID NOS: 19  
 23 <170> SOFTWARE: PatentIn version 3.3  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 3328  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Aspergillus nidulans  
 30 <400> SEQUENCE: 1

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35	ctgggcttgg	tatgagattg	cgagcatcta	tgtcggtgta	ccttctgaat	gacaatgaat	180
37	gtattttact	tctcgaaaaa	aacccttggg	cactgaattg	tgcggagaat	gatgccctga	240
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41	aaaatcgctt	gcacgaacag	acgaataacc	aagaaaaacg	ccgagcgcga	gcgtttcttc	360
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45	agaacttcag	ccctctgcat	cctgtcctta	ccgcaactcg	ttaacctgcg	cgacctcgcg	480
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49	actatcattc	tctgcattct	gagagtgate	tgtccttcga	cgttccttct	ttccagcgct	600
51	gcggcgccct	cactctcggt	gcctacgttt	gaccacggtc	ctacctctcc	tactgctgat	660
53	tattaggctc	ctccctacgc	ctccaatata	gggaagtcgc	cggccatggt	tcgtgcacga	720
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57	cgtctcgag	ttacgatcag	cctgcaatct	tgggtacctc	cgccgcccgt	cgatcaccat	840
59	aatccccctt	tccccgacca	gaacctcaaa	gatccatacg	aaaacgacaa	tagtgcgacc	900
61	ggcagtgagg	ctcctccgcc	tgcgttggta	gagccagaag	aataccaacg	accaccactt	960
63	tacacagatt	cagatgacag	cccaactccg	tcaaaagaac	gcctggacac	cccagacaa	1020
65	gtcccatctc	aggagcctga	atttgatgcc	gccagacttc	agacgggtgc	gcagacccaa	1080
67	aataaacatg	aagatgatga	ggatattgtc	ccaatttctc	actggaagcc	gatgcccga	1140
69	cggcatccag	tcagtccgga	ggctttgatc	aagcttgccaa	ccgggcaatc	aaaggaaactc	1200
71	ccccaaactg	aagctaagtt	caaggacag	tcgtcctcgg	acaagatgca	gcggctgcaa	1260
73	caacttgaca	ctatcaagtc	ggcgttctta	catgcgtgga	acggttataa	gatctctgcc	1320
75	atgggtcatg	atgaggttag	acctctgcgc	ggtggtttca	aggacacatt	caatggctgg	1380
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P.6

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79 tccatggcag tcgactacgt caagaaaatc gattttacca ccagcaccaa gaaagagatt 1500
81 ccggtctttg aaaccactat tcgctaccta ggcgggatgc tcggggccta tgatatttcg 1560
83 ggacacaaat acgatatact tttggaaaag tctgttgagc ttgcggatgt cttgatggac 1620
85 gccttcgaca caccgaaccg gatgccaaacc ctctattata aatggagccc agagtatgct 1680
87 tcagagtttc gccgggggga ctttaaggct gttctcgccg agcttggctc tctctctctc 1740
89 gagttcacgc gtttggcgca gttgacaaa caggacaagt actacgatgc aattgcacga 1800
91 atcacaaatg agctcgaaaa gtatcaggat ttgacaaagc ttcccggctt gtggcctctc 1860
93 aacctggacg catccgggtg caggcgagtt cccggcgctc cgcgagagcc tgctgcggct 1920
95 gggcagccag tcagatggtc ctctgacgag atcaactcga cgagctcggg atcgtatcgt 1980
97 acaagacaaa ttcattgaggg cggagagcct gtccgtcatg acaatgattc gtttgaaaacg 2040
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101 ctcaacgatc agctctcagg cattgacaag ttccgactcg gageccttgg tgactctacg 2160
103 tacgagtact taccgaaaga gtatatgttg ctccggcgga acaacgacca gtacctcaac 2220
105 atgtatcaga aggccatgga cacagtgcga gaatatcttg tttatcagcc aatgctcaag 2280
107 aataatcgcg atgtccgctt cttagcgaca gttagtatga caaagagcct tgatgcaaac 2340
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119 cctgaaaagg ggaattggca cgtcgctgcc acagccgaat cgtcttcgcc ccaggaagat 2700
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123 gcgctctcgc acgaggaatt cgtcacggga aaaatcctca acgaccgact cccgccgggc 2820
125 atgacaggga tctcggctcg gcagtacctc ctccgcccgg aggcgatcga gtctgtcttc 2880
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129 gctgtcgaca aagccacgaa gacggagctg gcgaactcgg ccatttccga cgtaaccgtc 3000
131 gataatccac gcccggtgga cagtatggaa tcattctggc ttgcggagac tctgaaatac 3060
133 ttctaccttc ttttcagcga tccaagcctg gtgagccttg acgaatatgt cttgtaagtg 3120
135 atgcttgact taatcgactg cttgatgctg acttttccct taggaacacc gaggctcatc 3180
137 cgttcaagcg acccaagtac tgaagtacta atttaaataga tcttttagcc tgatctata 3240
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146 <212> TYPE: DNA
147 <213> ORGANISM: Aspergillus nidulans
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151 <221> NAME/KEY: misc_feature
152 <222> LOCATION: (1632)..(1632)
153 <223> OTHER INFORMATION: n is a, g, c, or t/u
155 <400> SEQUENCE: 2
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160 cccgtcgatc accataatcc ccttttcccc gaccagaacc tcaaagatcc atacgaaaac 180
162 gacaatagtg cgaccggcag tggggctcct ccgcctgcgt tggtagagcc agaagaatac 240
164 caacgaccac cactttacac agattcagat gacagcccaa ctccgtcaaa agaacgcctg 300
166 gacaccccga gcaatgtccc atctcaggag cctgaatttg atgccgccag acttcagacg 360
168 ggtgcgacga cccaaaataa acatgaagat gatgaggata ttgtcccaat ttctcactgg 420
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176 tacaagatct ctgccatggg tcatgatgag gttagacctc tgcgcggtgg tttcaaggac 660
178 acattcaatg gctggggcgc gacccttgct gacgccttgg ataccctgtg gatcatggat 720
180 ctcaaagagg agttctccat ggcagtcgac tacgtcaaga aaatcgattt taccaccagc 780
182 accaagaaaag agattccggc ctttgaaacc actattcgct acctaggcgg gatgctcggg 840
184 gcctatgata tttcggggaca caaatacgat ataacttttg aaaagtctgt tgagcttgcg 900
186 gatgtcttga tggacgcctt cgacacaccg aaccggatgc caaccctcta ttataaatgg 960
188 agcccagagt atgcttcaga gtttcgccgg ggggacttta aggctgttct cgccgagctt 1020
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192 gatgcaattg cacgaatcac aaatgagctc gaaaagtatc aggatttgac aaagcttccc 1140
194 ggcttggtgg ctctcaacct ggacgcatcc ggggtgcaggc gagttcccgg cgtctcgcga 1200
196 gagcctgctg cggctgggca gccagtcaga tggctcctctg acgagatcaa ctgcacgagc 1260
198 tcggtatcgt atcgtacaag acaaattcat gagggcggag agcctgtccg tcatgacaat 1320
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206 gaccagtacc tcaacatgta tcagaaggcc atggacacag tgcgagaata tcttgtttat 1560
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212 tgttttgctg gtggtatgct tgccattggc gccaaagtgt ttgggcttga taaggatcta 1740
214 aagctgggta gtcaactgac ggacggctgt gtctgggcat atgaagccac aaagtccgga 1800
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218 gaggaacgat actacatggc catggatcct tatgccgaca agcggccaat atcacataac 1920
220 aaacgctccg ccggccctga aaaggggaat tggcacgtcg tcgccacagc cgaatcgtct 1980
222 tcgccccagg aagataaaac acagaaatca accactactg agggctcgaca caccggtaca 2040
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226 cgactccgcg cgggcatgac agggatctcg gctcggcagt acctccttcg cccggaggcg 2160
228 atcgagtctg tttcatcat gttecgctc acgggcgatc ctctctggcg cgaaaagggt 2220
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234 gagactctga aatacttcta ccttcttttc agcgatccaa gcctggtgag ccttgaggaa 2400
236 tatgtcttga acaccgaggc tcatccgttc aagcgacca ggtactga 2448

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239 &lt;210&gt; SEQ ID NO: 3

240 &lt;211&gt; LENGTH: 815

241 &lt;212&gt; TYPE: PRT

242 &lt;213&gt; ORGANISM: Aspergillus nidulans

244 &lt;400&gt; SEQUENCE: 3

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247 1 5 10 15
250 Phe Val Leu Leu Ile Phe His Phe Ser Arg Leu Ala Val Thr Ile Ser
251 20 25 30
254 Leu Gln Ser Trp Val Pro Pro Pro Pro Val Asp His His Asn Pro Pro
255 35 40 45
258 Phe Pro Asp Gln Asn Leu Lys Asp Pro Thr Glu Asn Asp Asn Ser Ala
259 50 55 60
262 Thr Gly Ser Gly Ala Pro Pro Pro Ala Leu Val Glu Pro Glu Glu Thr
263 65 70 75 80
266 Gln Arg Pro Pro Leu Thr Thr Asp Ser Asp Asp Ser Pro Thr Pro Ser

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267				85					90				95			
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271				100					105				110			
274	Phe	Asp	Ala	Ala	Arg	Leu	Gln	Thr	Gly	Ala	Gln	Thr	Gln	Asn	Lys	His
275			115					120					125			
278	Glu	Asp	Asp	Glu	Asp	Ile	Val	Pro	Ile	Ser	His	Trp	Lys	Pro	Met	Pro
279		130					135					140				
282	Glu	Arg	His	Pro	Val	Ser	Pro	Glu	Ala	Leu	Ile	Lys	Leu	Pro	Thr	Gly
283	145					150					155				160	
286	Gln	Ser	Lys	Glu	Leu	Pro	Gln	Leu	Gln	Ala	Lys	Phe	Lys	Asp	Glu	Ser
287				165					170					175		
290	Ser	Ser	Asp	Lys	Met	Gln	Arg	Leu	Gln	Gln	Leu	Asp	Thr	Ile	Lys	Ser
291				180					185					190		
294	Ala	Phe	Leu	His	Ala	Trp	Asn	Gly	Thr	Lys	Ile	Ser	Ala	Met	Gly	His
295			195				200						205			
298	Asp	Glu	Val	Arg	Pro	Leu	Arg	Gly	Gly	Phe	Lys	Asp	Thr	Phe	Asn	Gly
299		210					215					220				
302	Trp	Gly	Ala	Thr	Leu	Val	Asp	Ala	Leu	Asp	Thr	Leu	Trp	Ile	Met	Asp
303	225				230						235				240	
306	Leu	Lys	Glu	Glu	Phe	Ser	Met	Ala	Val	Asp	Thr	Val	Lys	Lys	Ile	Asp
307				245					250					255		
310	Phe	Thr	Thr	Ser	Thr	Lys	Lys	Glu	Ile	Pro	Val	Phe	Glu	Thr	Thr	Ile
311				260					265				270			
314	Arg	Thr	Leu	Gly	Gly	Met	Leu	Gly	Ala	Thr	Asp	Ile	Ser	Gly	His	Lys
315			275				280					285				
318	Thr	Asp	Ile	Leu	Leu	Glu	Lys	Ser	Val	Glu	Leu	Ala	Asp	Val	Leu	Met
319		290					295					300				
322	Asp	Ala	Phe	Asp	Thr	Pro	Asn	Arg	Met	Pro	Thr	Leu	Thr	Thr	Lys	Trp
323	305					310					315				320	
326	Ser	Pro	Glu	Thr	Ala	Ser	Glu	Phe	Arg	Arg	Gly	Asp	Phe	Lys	Ala	Val
327				325						330				335		
330	Leu	Ala	Glu	Leu	Gly	Ser	Leu	Ser	Leu	Glu	Phe	Thr	Arg	Leu	Ala	Gln
331				340					345				350			
334	Leu	Thr	Lys	Gln	Asp	Lys	Thr	Thr	Asp	Ala	Ile	Ala	Arg	Ile	Thr	Asn
335			355				360					365				
338	Glu	Leu	Glu	Lys	Thr	Gln	Asp	Leu	Thr	Lys	Leu	Pro	Gly	Leu	Trp	Pro
339		370					375				380					
342	Leu	Asn	Leu	Asp	Ala	Ser	Gly	Cys	Arg	Arg	Val	Pro	Gly	Val	Ser	Arg
343	385					390					395				400	
346	Glu	Pro	Ala	Ala	Ala	Gly	Gln	Pro	Val	Arg	Trp	Ser	Ser	Asp	Glu	Ile
347				405					410					415		
350	Asn	Ser	Thr	Ser	Ser	Val	Ser	Thr	Arg	Thr	Arg	Gln	Ile	His	Glu	Gly
351				420					425				430			
354	Gly	Glu	Pro	Val	Arg	His	Asp	Asn	Asp	Ser	Phe	Glu	Thr	Gly	Phe	Pro
355			435				440					445				
358	Val	Ser	Val	Asp	Thr	Arg	Thr	Pro	Pro	Pro	Lys	Gln	Asp	Cys	Thr	Gly
359		450					455				460					
362	Gly	Leu	Asn	Asp	Gln	Leu	Ser	Gly	Ile	Asp	Lys	Phe	Gly	Leu	Gly	Ala
363	465				470				475						480	

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371                               500                               505                               510
374 Thr Val Arg Glu Thr Leu Val Thr Gln Pro Met Leu Lys Asn Asn Arg
375                               515                               520                               525
378 Asp Val Arg Phe Leu Ala Thr Val Ser Met Thr Lys Ser Leu Asp Ala
379                               530                               535                               540
382 Asn Pro Pro Gly Arg Thr Thr Phe Ala Thr Glu Gly Thr His Leu Thr
383 545                               550                               555                               560
386 Cys Phe Ala Gly Gly Met Leu Ala Ile Gly Ala Lys Leu Phe Gly Leu
387                               565                               570                               575
390 Asp Lys Asp Leu Lys Leu Gly Ser Gln Leu Thr Asp Gly Cys Val Trp
391                               580                               585                               590
394 Ala Thr Glu Ala Thr Lys Ser Gly Ile Met Pro Glu Ala Phe Gln Leu
395                               595                               600                               605
398 Val Pro Cys Lys Lys Gly Glu Pro Cys Glu Trp Asp Glu Asp Ala Thr
399                               610                               615                               620
402 Thr Met Ala Met Asp Pro Thr Ala Asp Lys Arg Pro Ile Ser His Asn
403 625                               630                               635                               640
406 Lys Arg Ser Ala Gly Pro Glu Lys Gly Asn Trp His Val Val Ala Thr
407                               645                               650                               655
410 Ala Glu Ser Ser Ser Pro Gln Glu Asp Lys Thr Gln Lys Ser Thr Thr
411                               660                               665                               670
414 Thr Glu Gly Arg His Thr Gly Thr Thr Thr Gly Ala Gly Ala Leu Ser
415                               675                               680                               685
418 His Glu Glu Phe Val Thr Gly Lys Ile Leu Asn Asp Arg Leu Pro Pro
419                               690                               695                               700
422 Gly Met Thr Gly Ile Ser Ala Arg Gln Thr Leu Leu Arg Pro Glu Ala
423 705                               710                               715                               720
426 Ile Glu Ser Val Phe Ile Met Phe Arg Leu Thr Gly Asp Pro Ser Trp
427                               725                               730                               735
430 Arg Glu Lys Gly Trp Lys Met Phe Gln Ala Val Asp Lys Ala Thr Lys
431                               740                               745                               750
434 Thr Glu Leu Ala Asn Ser Ala Ile Ser Asp Val Thr Val Asp Asn Pro
435                               755                               760                               765
438 Arg Pro Val Asp Ser Met Glu Ser Phe Trp Leu Ala Glu Thr Leu Lys
439                               770                               775                               780
442 Thr Phe Thr Leu Leu Phe Ser Asp Pro Ser Leu Val Ser Leu Glu Glu
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452 <212> TYPE: DNA
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1652  
Seq#:8; N Pos. 4  
Seq#:15; N Pos. 9,18  
Seq#:16; N Pos. 4,13,16,22,25

**VERIFICATION SUMMARY**

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Input Set : A:\62447-01.ST25.txt

Output Set: N:\CRF4\11092004\J089211B.raw

L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1620  
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0